2007

Insect-mediated Cross-pollination in Soybean [Glycine max (L.) Merrill]: II. Phenotypic Recurrent Selection

E. Ortiz-Perez
Iowa State University

H. Wiley
Dairyland Seed Co., Inc.

Harry T. Horner
Iowa State University, hth@iastate.edu

W. H. Davis
Verde Seeds, Inc.

R. G. Palmer
U.S. Department of Agriculture

Insect-mediated Cross-pollination in Soybean [Glycine max (L.) Merrill]: II. Phenotypic Recurrent Selection

Abstract

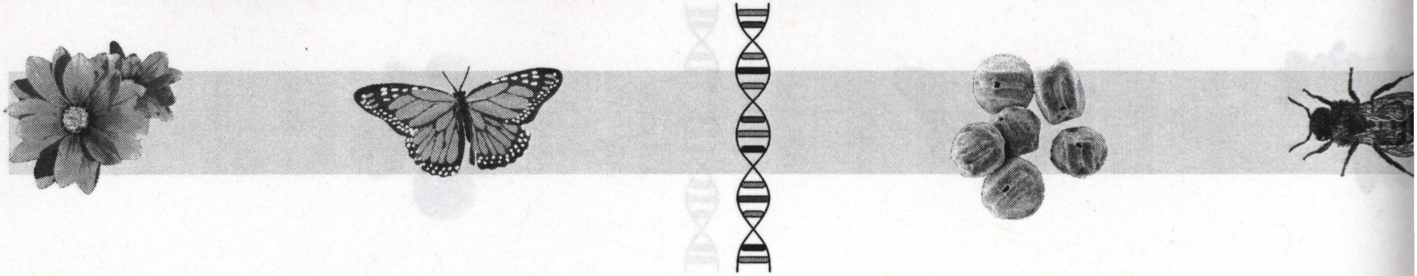
Recurrent selection (RS) includes the systematic selection of desirable individuals from a population followed by recombination of the selected individuals to form a new population [l]. Nuclear male-sterility with insect-mediated cross-pollination has been successfully used in RS schemes in soybean [Glycine max (L.) Merrill]. However, selection to increase the seed-set on male-sterile plants per se has received minimal attention. Preferential pollination observed through seed-set suggested that selection on male-sterile plants for high seed-set can be attained [2, 3]. Thus, selected male-sterile, female-fertile lines could be suitable to produce larger amounts of hybrid soybean seed.

Disciplines

Agriculture | Entomology | Plant Biology | Plant Breeding and Genetics

Comments

This poster is from Ortiz-Perez E, H Wiley, HT Horner, WH Davis, and RG Palmer. 2007. Insect-mediated cross-pollination in coybean [*Glycine max* (L.) Merrill]: II. Phenotypic recurrent selection. 9th International Pollination Symposium on Plant-Pollinator Relationships—Diversity in Action. pp. 178-179. Iowa State University, Ames, IA USA (June 25-28).



Insect-mediated Cross-pollination in Soybean [*Glycine max* (L.) Merrill]: II. Phenotypic Recurrent Selection

E. Ortiz-Perez
Department of Agronomy
Iowa State University, Ames, IA 50011 USA
E-mail: evelynortiz_perez@yahoo.com

H. Wiley
Dairyland Seed Co., Inc.
Otterbein, IN 47970 USA

H.T. Horner
Department of Genetics, Development and Cell Biology
and Microscopy and NanoImaging Facility
Iowa State University, Ames, IA 50011 USA

W.H. Davis
Verde Seeds, Inc.
Plainview, TX 79072 USA

R.G. Palmer
USDA-ARS-CICGR and Department of Agronomy
Iowa State University, Ames, IA 50011 USA

Recurrent selection (RS) includes the systematic selection of desirable individuals from a population followed by recombination of the selected individuals to form a new population [1]. Nuclear male-sterility with insect-mediated cross-pollination has been successfully used in RS schemes in soybean [*Glycine max* (L.) Merrill] However, selection to increase the seed-set on male-sterile plants *per se* has received minimal attention. Preferential pollination observed through seed-set suggested that selection on male-sterile plants for high seed-set can be attained [2, 3]. Thus, selected male-sterile, female-fertile lines could be suitable to produce larger amounts of hybrid soybean seed. The objective of this study was to evaluate the response of male-sterile lines segregating for male-sterile alleles *ms2*, *ms3*, *ms6*, *ms8*, and *ms9* to phenotypic recurrent selection for increased seed-set, using a selected group of male parents. Data were obtained from plots at Plainview, Texas, in 2003, 2004, and 2005. Bees from families Halictidae, Anthophoridae, Andrenidae, and Megachilidae were utilized as pollinator vectors. Three generations of backcrossing, and two-way, three-way, four-way, and five-way crosses were evaluated. For the BC strategy, male-sterile plants presented from 42 to 80% of the normal seed-set observed in fertile normal plants from the same background, which is higher than previous reports in the literature. Three-way, four-way, and five-way crosses presented a higher seed-set compared to BC generations (Figure 1). Nonetheless, both, the BC strategy and adding a new male parent each cycle were effective to increase the mean seed-set across populations (Table 1). More homogeneous lines were observed in the BC strategy compared to the populations with a background where five parents are expected to segregate for those traits. Although a differential response was observed among populations, the seed-set observed would justify the use of some specific male-sterile selections as female parents in a hybrid soybean seed production system.

References

[1] Fehr, W.R. (1991) *Principles of cultivar development. Theory and technique.* Macmillan Publishing Co. Ames, IA.

[2] Lewers, K.S., and R.G. Palmer. (1997) Recurrent selection in soybean. *Plant Breed. Rev.* 15:275–313.

[3] Ortiz-Perez, E., H.T. Horner, S.J. Hanlin, and R.G. Palmer. (2006) Insect-mediated seed set evaluation among 21 soybean lines segregating for male sterility at 10 different loci. *Euphytica* 152:351–360.

Figure 1. High seed-set four-way cross [A00-39 *ms2*) × Corsoy 79 × DSR Exp. 202b] × GH 4190

Table 1. Maximum (Max) and minimum (Min) number of seed/soybean family for each population within three-way, four-way, five-way, BC_1, BC_2, and BC_3 crosses. Texas data.

Population	Mean Seed No./Male-sterile Family					
	2003		2004		2005	
	Common Male 1*		Common Male 2**		Common Male 3***	
	Three-way Cross		Four-way Cross		Five-way Cross	
Female Parent	**Max**	**Min**	**Max**	**Min**	**Max**	**Min**
(A00-39 *ms2* × Corsoy 79)	174	61	465	244	190	142
(A00-39 *ms2* × Hark)	316	57	330	6	246	68
(A00-41 *ms2* × A00-73 *Ms9*)	195	27	337	94	227	88
[A00-63 *ms2* (Beeson) × Wells]	84	8	297	228	151	126
(A00-68 *ms3* × A00-41 *Ms2*)	187	49	263	78	252	224
(A00-72 *ms8* × A00-68 *Ms3*)	159	68	329	147	238	152
(A00-73 *ms9* v Raiden)	173	6	266	38	251	172
[A94-20×19(*ms6*) × A00-39 *Ms2*]	104	24	232	63	177	104

* DSR Exp. 202b, ** GH 4190, *** DSR Exp. 202c

Population	BC_1		BC_2		BC_3	
Female Parent	**Max**	**Min**	**Max**	**Min**	**Max**	**Min**
(A00-39 *ms2* × Corsoy 79)	198	17	201	49	161	45
(A00-39 *ms2* × Hark)	219	33	271	73	214	22
(A00-41 *ms2* × A00-73 *Ms9*)	142	35	269	3	165	24
[A00-63 *ms2* (Beeson) × Wells]	95	18	140	36	108	87
(A00-68 *ms3* × A00-41 *Ms2*)	176	28	482	75	313	144
(A00-72 *ms8* × A00-68 *Ms3*)	45	26	ND		ND	
(A00-73 *ms9* × Raiden)	234	13	241	67	261	180
[A94-20×19(*ms6*) × A00-39 *Ms2*]	137	33	245	10	190	134

ND = No data